```
==============================================================
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2010; month=4; day=14; hr=14; min=23; sec=10; ms=231; ]
==============================================================
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Application No: 10581014   Version No: 1.0

Input Set:

Output Set:

Started: 2010-04-05 18:02:15.979
Finished: 2010-04-05 18:02:39.014
Elapsed: 0 hr(s) 0 min(s) 23 sec(s) 35 ms
Total Warnings: 629
Total Errors: 34
No. of SeqIDs Defined: 711
Actual SeqID Count: 711

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (15)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (15)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)

```
              Input Set:


             Output Set:



               Started:   2010-04-05 18:02:15.979
              Finished:   2010-04-05 18:02:39.014
               Elapsed:   0 hr(s) 0 min(s) 23 sec(s) 35 ms
        Total Warnings:   629
          Total Errors:   34
  No. of SeqIDs Defined:   711
     Actual SeqID Count:   711


 Error code        Error Description


W   213       Artificial or Unknown found in <213>  in SEQ ID (29)

W   213       Artificial or Unknown found in <213>  in SEQ ID (30)

W   213       Artificial or Unknown found in <213>  in SEQ ID (31)

W   213       Artificial or Unknown found in <213>  in SEQ ID (32)

W   213       Artificial or Unknown found in <213>  in SEQ ID (33)

W   213       Artificial or Unknown found in <213>  in SEQ ID (34)
               This error has occured more than 20 times, will not be displayed

W   402       Undefined organism found in <213>  in SEQ ID (96)

W   402       Undefined organism found in <213>  in SEQ ID (97)

E   355       Empty lines found between the amino acid numbering and the

E   321       No. of Bases conflict, this line has no nucleotides  SEQID (99)

E   355       Empty lines found between the amino acid numbering and the

E   321       No. of Bases conflict, this line has no nucleotides  SEQID (103)

W   402       Undefined organism found in <213>  in SEQ ID (112)

W   402       Undefined organism found in <213>  in SEQ ID (113)

W   402       Undefined organism found in <213>  in SEQ ID (118)

W   402       Undefined organism found in <213>  in SEQ ID (119)

W   402       Undefined organism found in <213>  in SEQ ID (132)

E   355       Empty lines found between the amino acid numbering and the

E   321       No. of Bases conflict, this line has no nucleotides  SEQID (646)

W   402       Undefined organism found in <213>  in SEQ ID (648)

W   402       Undefined organism found in <213>  in SEQ ID (653)

W   402       Undefined organism found in <213>  in SEQ ID (654)
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              Input Set:


              Output Set:



          Started:    2010-04-05 18:02:15.979
         Finished:    2010-04-05 18:02:39.014
          Elapsed:    0 hr(s) 0 min(s) 23 sec(s) 35 ms
   Total Warnings:    629
     Total Errors:    34
No. of SeqIDs Defined:    711
Actual SeqID Count:    711
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Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (654)
W 402	Undefined organism found in <213> in SEQ ID (656)
W 402	Undefined organism found in <213> in SEQ ID (663)
W 402	Undefined organism found in <213> in SEQ ID (666)
W 402	Undefined organism found in <213> in SEQ ID (671)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (671)
W 402	Undefined organism found in <213> in SEQ ID (677)
W 402	Undefined organism found in <213> in SEQ ID (683)
W 402	Undefined organism found in <213> in SEQ ID (684)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (684)
W 402	Undefined organism found in <213> in SEQ ID (688)
	This error has occured more than 20 times, will not be displayed
E 341	'Xaa' position not defined SEQID (701) POS (168)
E 341	'Xaa' position not defined SEQID (701) POS (169)
E 341	'Xaa' position not defined SEQID (701) POS (170)
E 341	'Xaa' position not defined SEQID (701) POS (171)
E 341	'Xaa' position not defined SEQID (701) POS (172)
E 341	'Xaa' position not defined SEQID (701) POS (173)
E 341	'Xaa' position not defined SEQID (701) POS (174)
E 341	'Xaa' position not defined SEQID (701) POS (175)

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       Input Set:


       Output Set:



              Started:   2010-04-05 18:02:15.979
             Finished:   2010-04-05 18:02:39.014
              Elapsed:   0 hr(s) 0 min(s) 23 sec(s) 35 ms
      Total Warnings:    629
        Total Errors:    34
No. of SeqIDs Defined:   711
   Actual SeqID Count:   711
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Error code   Error Description

E   341   'Xaa' position not defined   SEQID (701)   POS (176)

E   341   'Xaa' position not defined   SEQID (701)   POS (177)

E   341   'Xaa' position not defined   SEQID (701)   POS (178)

E   341   'Xaa' position not defined   SEQID (701)   POS (179)

E   341   'Xaa' position not defined   SEQID (701)   POS (180)

E   341   'Xaa' position not defined   SEQID (701)   POS (181)

E   341   'Xaa' position not defined   SEQID (701)   POS (182)

E   341   'Xaa' position not defined   SEQID (701)   POS (183)

E   341   'Xaa' position not defined   SEQID (701)   POS (184)

E   341   'Xaa' position not defined   SEQID (701)   POS (185)

atggccaagc gaattctgtg tttcggtgat tccctgacct ggggctgggt ccccgtcgaa   60

gacggggcac ccaccgagcg gttcgccccc gacgtgcgct ggaccggtgt gctggcccag   120

cagctcggag cggacttcga ggtgatcgag gagggactga gcgcgcgcac caccaacatc   180

gacgacccca ccgatccgcg gctcaacggc gcgagctacc tgccgtcgtg cctcgcgacg   240

cacctgccgc tcgacctggt gatcatcatg ctgggcacca acgacaccaa ggcctacttc   300

cggcgcaccc cgctcgacat cgcgctgggc atgtcggtgc tcgtcacgca ggtgctcacc   360

agcgcgggcg gcgtcggcac cacgtacccg gcacccaagg tgctggtggt ctcgccgcca   420

ccgctggcgc ccatgccgca cccctggttc cagttgatct tcgagggcgg cgagcagaag   480

accactgagc tcgcccgcgt gtacagcgcg ctcgcgtcgt tcatgaaggt gccgttcttc   540

gacgcgggtt cggtgatcag caccgacggc gtcgacggaa tccacttcac cgaggccaac   600

aatcgcgatc tcggggtggc cctcgcggaa caggtgcgga gcctgctgta a   651

<210>   2
<211>   216
<212>   PRT
<213>   Mycobacterium smegmatis

<400>   2

Met Ala Lys Arg Ile Leu Cys Phe Gly Asp Ser Leu Thr Trp Gly Trp
1   5   10   15

Val Pro Val Glu Asp Gly Ala Pro Thr Glu Arg Phe Ala Pro Asp Val
            20   25   30

Arg Trp Thr Gly Val Leu Ala Gln Gln Leu Gly Ala Asp Phe Glu Val
        35   40   45

Ile Glu Glu Gly Leu Ser Ala Arg Thr Thr Asn Ile Asp Asp Pro Thr
    50   55   60

Asp Pro Arg Leu Asn Gly Ala Ser Tyr Leu Pro Ser Cys Leu Ala Thr
65   70   75   80

His Leu Pro Leu Asp Leu Val Ile Ile Met Leu Gly Thr Asn Asp Thr
                85   90   95

Lys Ala Tyr Phe Arg Arg Thr Pro Leu Asp Ile Ala Leu Gly Met Ser
                100   105   110

Val Leu Val Thr Gln Val Leu Thr Ser Ala Gly Gly Val Gly Thr Thr
            115   120   125

Tyr Pro Ala Pro Lys Val Leu Val Val Ser Pro Pro Pro Leu Ala Pro
    130   135   140

Met Pro His Pro Trp Phe Gln Leu Ile Phe Glu Gly Gly Glu Gln Lys
145   150   155   160

Thr Thr Glu Leu Ala Arg Val Tyr Ser Ala Leu Ala Ser Phe Met Lys
                165   170   175

Val Pro Phe Phe Asp Ala Gly Ser Val Ile Ser Thr Asp Gly Val Asp
                180   185   190

Gly Ile His Phe Thr Glu Ala Asn Asn Arg Asp Leu Gly Val Ala Leu
        195   200   205

Ala Glu Gln Val Arg Ser Leu Leu
    210   215

```
<210>  3
<211>  19
<212>  PRT
<213>  Mycobacterium parafortuitum


<400>  3

Lys Val Pro Phe Phe Asp Ala Gly Ser Val Ile Ser Thr Asp Gly Val
1               5                   10                  15

Asp Gly Ile


<210>  4
<211>  19
<212>  PRT
<213>  Mycobacterium parafortuitum


<400>  4

Gly Thr Arg Arg Ile Leu Ser Phe Gly Asp Ser Leu Thr Trp Gly Trp
1               5                   10                  15

Ile Pro Val


<210>  5
<211>  59
<212>  DNA
<213>  Artificial Sequence


<220>
<223>  primer


<400>  5
ctaacaggag gaattaacca tggccaagcg aattctgtgt ttcggtgatt ccctgacct        59


<210>  6
<211>  59
<212>  DNA
<213>  Artificial Sequence


<220>
<223>  primer


<400>  6
gcgcgcggat ccgcgcgctt acagcaggct ccgcacctgt tccgcgaggg ccacccgga        59


<210>  7
<211>  10
<212>  DNA
<213>  Mycobacterium smegmatis


<400>  7
ggctggggggc                                                             10


<210>  8
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<211> 1779

<212> DNA

<213> Mycobacterium smegmatis

<400> 8

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ggatgttcgt cgtccccgga tccggccgac cggttctcgg cgttcgccga ggcgctgggc   120

cgcaaggatg cggccgcggc ggccgcccag accagcgatc cggcggccgc ggaggcggcc   180

atcaccgcga tgctggccgg gatgggcgac gccgcgaacg tctcggtggc cgccgaaccc   240

gaggaaggcg acgacgcggg cgcgacgctg aagtacacgt ggacctgggg tgagggccgc   300

gacttcggct acgacaccac cgcgacggcg gccaaatccg gtgacgactg gctgatcacc   360

tggtccccca ccgtgttgca ccgcgacctc accccggatc tgcgcttcca gtacagcgag   420

gacagcgaat gcagacccc ggtgctcgac cgcaccggcc agccgttgat gacatggcag   480

accgtcggtg tcatcactgt cgaacgcgca catccggagt cggccgcacc gctcgccgcc   540

ctgctggcgc ccttcgatcc gaccaccacc accgaatcgg tcaccgcaca actcaattcg   600

acgaccgatg accgcgtgac ggtgatgaag ctgcgcgagg acgatctggg tcaggtgcgc   660

gatcagctcg cgcagatccc cggcgtgacc gtgcgtgagc agggtgagct gctcaccgcc   720

gaccggcagc tgtcctcgcc cgccatcagc ggcctggacg agctgtggca cgaccggatc   780

accgccaacg cgggctggtc ggtgtacctg gtcgacgccg acggtgcacc cgcacaacag   840

ctcacgtcca cgccgcccaa ggacaccggg cccgtgcgca ccacgctgga cctgcgcatg   900

caactgctcg cgcagcaggc cgtggccaag gagacccgcc cggccgtggt ggtcgcgatc   960

tccggatcga ccgggggcat cctggccgcc gcacagaacc cggccgccga tccgcaaggt   1020

gcgatcgcgt tttcgggcct gtacccgccg gggtcgacgt tcaagaccat caccacggcg   1080

gcagccctcg acgcgggcct ggccacccg gacacaccgg tggcctgccc gggtgagctc   1140

accatcgaga accgcacgat ccccaacgac gacaacttcg acctgggcac cgtgccgttg   1200

tcgtcggcgt tctcgcactc ctgcaacacc agcatggccg ccctgtccga cgagctgccg   1260

cccaacgcac tgaccgacat ggcaaaggac ttcgggatcg gcgtcgactt catggtgccc   1320

ggcctgacca ccgtgaccgg ccgtgtcccc aacgccgaca cgccgcccca gcgtgtcgag   1380

aacggcatcg gccagggcac cgtgaccgtc agcccgttcg gcctcgccgt cgccgaggcc   1440

agcctggcgc acggttcgac gatcctgccg acgctggtcg acggcgagaa gaccacggcc   1500

gacaccccgt cggtgccgtt gccgcccaac atcaccgacg cgctgcgcgc gatgatgcgc   1560

ggaacggtca ccgagggcac ggccaccgcg ttgagcgaca tccccgacct gggcggcaag   1620

accggcacgg cggaattcgg cgacaacacg cactcgcacg ctggttcgc gggcatcgcg   1680

ggcgacatcg cgttcgcgac gctggtggtc ggcggcgact cgtcggcacc ggccgtcgcg   1740

atctcaggag acttcctgcg ccccgcgctc gccggctag   1779

<210> 9
<211> 592
<212> PRT
<213> Mycobacterium smegmatis

<400> 9

Met His Leu Arg Pro Ala Leu Thr Trp Leu Leu Val Val Gly Leu Phe
1   5   10   15

Ile Ser Val Val Gly Cys Ser Ser Ser Pro Asp Pro Ala Asp Arg Phe
            20   25   30

Ser Ala Phe Ala Glu Ala Leu Gly Arg Lys Asp Ala Ala Ala Ala Ala
        35   40   45

Ala Gln Thr Ser Asp Pro Ala Ala Ala Glu Ala Ala Ile Thr Ala Met
    50   55   60

Leu Ala Gly Met Gly Asp Ala Ala Asn Val Ser Val Ala Ala Glu Pro
65   70   75   80

Glu Glu Gly Asp Asp Ala Gly Ala Thr Leu Lys Tyr Thr Trp Thr Trp
                85   90   95

Gly Glu Gly Arg Asp Phe Gly Tyr Asp Thr Thr Ala Thr Ala Ala Lys
            100   105   110

Ser Gly Asp Asp Trp Leu Ile Thr Trp Ser Pro Thr Val Leu His Arg
        115   120   125

Asp Leu Thr Pro Asp Leu Arg Phe Gln Tyr Ser Glu Asp Ser Glu Leu
    130   135   140

Gln Thr Pro Val Leu Asp Arg Thr Gly Gln Pro Leu Met Thr Trp Gln
145   150   155   160

Thr Val Gly Val Ile Thr Val Glu Arg Ala His Pro Glu Ser Ala Ala
                165   170   175

Pro Leu Ala Ala Leu Leu Ala Pro Phe Asp Pro Thr Thr Thr Thr Glu
            180   185   190

Ser Val Thr Ala Gln Leu Asn Ser Thr Thr Asp Asp Arg Val Thr Val
        195   200   205

Met Lys Leu Arg Glu Asp Asp Leu Gly Gln Val Arg Asp Gln Leu Ala
    210   215   220

```
Gln Ile Pro Gly Val Thr Val Arg Glu Gln Gly Glu Leu Leu Thr Ala
225                 230             235                     240

Asp Arg Gln Leu Ser Ser Pro Ala Ile Ser Gly Leu Asp Glu Leu Trp
            245             250                 255

His Asp Arg Ile Thr Ala Asn Ala Gly Trp Ser Val Tyr Leu Val Asp
            260             265             270

Ala Asp Gly Ala Pro Ala Gln Gln Leu Thr Ser Thr Pro Pro Lys Asp
            275             280             285

Thr Gly Pro Val Arg Thr Thr Leu Asp Leu Arg Met Gln Leu Leu Ala
    290             295                 300

Gln Gln Ala Val Ala Lys Glu Thr Arg Pro Ala Val Val Val Ala Ile
305             310             315                     320

Ser Gly Ser Thr Gly Gly Ile Leu Ala Ala Ala Gln Asn Pro Ala Ala
                325             330                 335

Asp Pro Gln Gly Ala Ile Ala Phe Ser Gly Leu Tyr Pro Pro Gly Ser
            340             345                 350

Thr Phe Lys Thr Ile Thr Thr Ala Ala Ala Leu Asp Ala Gly Leu Ala
        355             360                 365

Thr Pro Asp Thr Pro Val Ala Cys Pro Gly Glu Leu Thr Ile Glu Asn
    370             375                 380

Arg Thr Ile Pro Asn Asp Asp Asn Phe Asp Leu Gly Thr Val Pro Leu
385             390                 395                     400

Ser Ser Ala Phe Ser His Ser Cys Asn Thr Ser Met Ala Ala Leu Ser
                405                 410                 415

Asp Glu Leu Pro Pro Asn Ala Leu Thr Asp Met Ala Lys Asp Phe Gly
            420                 425                 430

Ile Gly Val Asp Phe Met Val Pro Gly Leu Thr Thr Val Thr Gly Arg
        435                 440                 445

Val Pro Asn Ala Asp Asn Ala Ala Gln Arg Val Glu Asn Gly Ile Gly
    450                 455                 460

Gln Gly Thr Val Thr Val Ser Pro Phe Gly Leu Ala Val Ala Glu Ala
465                 470                 475                     480

Ser Leu Ala His Gly Ser Thr Ile Leu Pro Thr Leu Val Asp Gly Glu
                485                 490                 495

Lys Thr Thr Ala Asp Thr Pro Ser Val Pro Leu Pro Pro Asn Ile Thr
            500                 505                 510

Asp Ala Leu Arg Ala Met Met Arg Gly Thr Val Thr Glu Gly Thr Ala
    515                 520                 525
```

Thr Ala Leu Ser Asp Ile Pro Asp Leu Gly Gly Lys Thr Gly Thr Ala
    530   535   540

Glu Phe Gly Asp Asn Thr His Ser His Gly Trp Phe Ala Gly Ile Ala
545   550   555   560

Gly Asp Ile Ala Phe Ala Thr Leu Val Val Gly Gly Asp Ser Ser Ala
                565   570   575

Pro Ala Val Ala Ile Ser Gly Asp Phe Leu Arg Pro Ala Leu Ala Gly
            580   585   590

<210>   10
<211>   592
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   penicillin binding protein

<400>   10

Met His Leu Arg Pro Ala Leu Thr Trp Leu Leu Val Val Gly Leu Phe
1   5   10   15

Ile Ser Val Val Gly Cys Ser Ser Ser Pro Asp Pro Ala Asp Arg Phe
                20   25   30

Ser Ala Phe Ala Glu Ala Leu Gly Arg Lys Asp Ala Ala Ala Ala Ala
            35   40   45

Ala Gln Thr Ser Asp Pro Ala Ala Ala Glu Ala Ala Ile Thr Ala Met
    50   55   60

Leu Ala Gly Met Gly Asp Ala Ala Asn Val Ser Val Ala Ala Glu Pro
65   70   75   80

Glu Glu Gly Asp Asp Ala Gly Ala Thr Leu Lys Tyr Thr Trp Thr Trp
                85   90   95

Gly Glu Gly Arg Asp Phe Gly Tyr Asp Thr Thr Ala Thr Ala Ala Lys
                100   105   110

Ser Gly Asp Asp Trp Leu Ile Thr Trp Ser Pro Thr Val Leu His Arg
            115   120   125

Asp Leu Thr Pro Asp Leu Arg Phe Gln Tyr Ser Glu Asp Ser Glu Leu
    130   135   140

Gln Thr Pro Val Leu Asp Arg Thr Gly Gln Pro Leu Met Thr Trp Gln
145   150   155   160

Thr Val Gly Val Ile Thr Val Glu Arg Ala His Pro Glu Ser Ala Ala
                165   170   175

Pro Leu Ala Ala Leu Leu Ala Pro Phe Asp Pro Thr Thr Thr Thr Glu

```
                 180                      185                      190

Ser Val Thr Ala Gln Leu Asn Ser Thr Thr Asp Asp Arg Val Thr Val
    195                      200                      205

Met Lys Leu Arg Glu Asp Asp Leu Gly Gln Val Arg Asp Gln Leu Ala
    210                      215                      220

Gln Ile Pro Gly Val Thr Val Arg Glu Gln Gly Glu Leu Leu Thr Ala
225                      230                      235                      240

Asp Arg Gln Leu Ser Ser Pro Ala Ile Ser Gly Leu Asp Glu Leu Trp
                 245                      250                      255

His Asp Arg Ile Thr Ala Asn Ala Gly Trp Ser Val Tyr Leu Val Asp
                 260                      265                      270

Ala Asp Gly Ala Pro Ala Gln Gln Leu Thr Ser Thr Pro Pro Lys Asp
                 275                      280                      285

Thr Gly Pro Val Arg Thr Thr Leu Asp Leu Arg Met Gln Leu Leu Ala
    290                      295                      300

Gln Gln Ala Val Ala Lys Glu Thr Arg Pro Ala Val Val Val Ala Ile
305                      310                      315                      320

Ser Gly Ser Thr Gly Gly Ile Leu Ala Ala Ala Gln Asn Pro Ala Ala
                 325                      330                      335

Asp Pro Gln Gly Ala Ile Ala Phe Ser Gly Leu Tyr Pro Pro Gly Ser
                 340                      345                      350

Thr Phe Lys Thr Ile Thr Thr Ala Ala Ala Leu Asp Ala Gly Leu Ala
                 355                      360                      365

Thr Pro Asp Thr Pro Val Ala Cys Pro Gly Glu Leu Thr Ile Glu Asn
    370                      375                      380

Arg Thr Ile Pro Asn Asp Asp Asn Phe Asp Leu Gly Thr Val Pro Leu
385                      390                      395                      400

Ser Ser Ala Phe Ser His Ser Cys Asn Thr Ser Met Ala Ala Leu Ser
                 405                      410                      415

Asp Glu Leu Pro Pro Asn Ala Leu Thr Asp Met Ala Lys Asp Phe Gly
                 420                      425                      430

Ile Gly Val Asp Phe Met Val Pro Gly Leu Thr Thr Val Thr Gly Arg
    435                      440                      445

Val Pro Asn Ala Asp Asn Ala Ala Gln Arg Val Glu Asn Gly Ile Gly
    450                      455                      460

Gln Gly Thr Val Thr Val Ser Pro Phe Gly Leu Ala Val Ala Glu Ala
465                      470                      475                      480

Ser Leu Ala His Gly Ser Thr Ile Leu Pro Thr Leu Val Asp Gly Glu
```

```
                    485                 490                 495
Lys Thr Thr Ala Asp Thr Pro Ser Val Pro Leu Pro Pro Asn Ile Thr
            500                 505                 510

Asp Ala Leu Arg Ala Met Met Arg Gly Thr Val Thr Glu Gly Thr Ala
        515                 520                 525

Thr Ala Leu Ser Asp Ile Pro Asp Leu Gly Gly Lys Thr Gly Thr Ala
    530                 535                 540

Glu Phe Gly Asp Asn Thr His Ser His Gly Trp Phe Ala Gly Ile Ala
545                 550                 555                 560

Gly Asp Ile Ala Phe Ala Thr Leu Val Val Gly Gly Asp Ser Ser Ala
                565                 570                 575

Pro Ala Val Ala Ile Ser Gly Asp Phe Leu Arg Pro Ala Leu Ala Gly
            580                 585                 590
```

```
<210>   11
<211>   43
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   11
atgggtaccc gacgaattct gtccttcggt gattccctga cct                       43


<210>   12
<211>   51
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   12
gattccgtcg acgccgtcgg tgctgatcac cgaacccgcg tcgaagaacg g             51


<210>   13
<211>   4189
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   pMSATNcoI plasmid

<400>   13
agcgcccaat acgcaaaccg cctctccccg cgcgttggcc gattcattaa tgcagctggc    60

acgacaggtt tcccgactgg aaagcgggca gtgagcgcaa cgcaattaat gtgagttagc    120

tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa    180
```

```
ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac gccaagctat      240

ttaggtgaca ctatagaata ctcaagctat gcatcaagct tggtaccgag ctcggatcca      300

ctagtaacgg ccgccagtgt gctggaattc gcccttctaa caggaggaat taaccatggc      360

caagcgaatt ctgtgtttcg gtgattccct gacctggggc tgggtccccg tcgaagacgg      420

ggcacccacc gagcggttcg cccccgacgt gcgctggacc ggtgtgctgg cccagcagct      480

cggagcggac ttcgaggtga tcgaggaggg actgagcgcg cgcaccacca acatc
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